

VIEWING THE SEQUENCE INFORMATION FOR THE PROTEIN Q847D1\_NODSP



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Protein Q847D1\_NODSP



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General information about the UniProt/TrEMBL entry	
Entry name	Q847D1_NODSP
Primary accession number	Q847D1
Entered in TrEMBL	Release 24, 01-JUN-2003
Sequence was last modified	Release 24, 01-JUN-2003
Annotations were last modified	Release 26, 01-MAR-2004
Protein description	
Protein name	Putative beta-carotene ketolase
Origin of the protein	
From	Nodularia spumigena[TaxID:70799]
Taxonomy	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nodularia.
References	
[1]	NUCLEOTIDE SEQUENCE. STRAIN=NSOR10; DOI=10.1007/s00239-002-2415-0; MEDLINE=22549861; PubMed=12664164; [NCBI, ExPASy, EBI, Israel, Japan] Moffitt M.C., Neilan B.A.; "Evolutionary affiliations within the superfamily of ketosynthases reflect complex pathway associations". J. Mol. Evol. 56:446-457(2003).
[2]	NUCLEOTIDE SEQUENCE.

STRAIN=NSOR10; DOI=10.1128/AEM.70.11.6353-6362.2004; PubMed=15528492; [NCBI, ExpASY, EBI, Israel, Japan] Moffitt M.C., Neilan B.A.; "Characterization of the nodularin synthetase gene cluster and proposed theory of the evolution of cyanobacterial hepatotoxins."; Appl. Environ. Microbiol. 70:6353-6362(2004).																					
Cross-references																					
EMBL	AY210783; AAO64399.1; -; Genomic_DNA.[EMBL/ GenBank/ DDBJ] [CoDingSequence]																				
GO	<table><tr><td>Cellular component</td><td>membrane</td><td>GO:0016020</td><td>inferred from electronic annotation</td></tr><tr><td>Molecular function</td><td>oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water</td><td>GO:0016717</td><td>inferred from electronic annotation</td></tr><tr><td>Molecular function</td><td>oxidoreductase activity, acting on single donors with incorporation of molecular oxygen</td><td>GO:0016701</td><td>inferred from electronic annotation</td></tr><tr><td>Biological process</td><td>carotene metabolism</td><td>GO:0016119</td><td>inferred from electronic annotation</td></tr><tr><td>Biological process</td><td>fatty acid desaturation</td><td>GO:0006636</td><td>inferred from electronic annotation</td></tr></table> <div>[QuickGO]</div>	Cellular component	membrane	GO:0016020	inferred from electronic annotation	Molecular function	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	GO:0016717	inferred from electronic annotation	Molecular function	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0016701	inferred from electronic annotation	Biological process	carotene metabolism	GO:0016119	inferred from electronic annotation	Biological process	fatty acid desaturation	GO:0006636	inferred from electronic annotation
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Molecular function	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0016701	inferred from electronic annotation																		
Biological process	carotene metabolism	GO:0016119	inferred from electronic annotation																		
Biological process	fatty acid desaturation	GO:0006636	inferred from electronic annotation																		
InterPro	IPR011393; Carotene_ketolas. IPR005804; Fa_desat. IPR010257; FA_desat_sub. Graphical view of the domain structure																				
Pfam	PF00487; FA_desaturase; 1. Pfam graphical view of domain structure																				
PIRSF	PIRSF027840; Carotene_ketolas; 1.																				
ProDom	PD001081; FA_desat_sub; 1. [Domain structure/ List of seq. sharing at least 1 domain]																				
Sequence information																					
Length	229 AA																				
Molecular weight	27832 Da																				

CRC64	71C9271BB371C95B	[This is a checksum on the sequence]
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MAIAIISIWA	ISQFKFWMLL	PLIFWQTFLY TGLFITAHDA 50
MHGUVFPKNP	KINHFIGSLC	LFLYGLLPYQ KLLKKHWWLHH HNPASETDPD 100
FHNGKQKNFF	AWLYLFMKRY	WSWLQIIITLM IINYLLKYIW HPFEDNMTYF 150
WVVPSTILSSL	QLFYFCTFLP	HSEPVEGYKE PHRSQTISR P IWSFSITCYH 200
FGYHYEHHEY	PHVPWWQLPE	IYKMSKSNL 229